1	MPMPSRDGGLHPRHHHYGSHSPWSQLLSSPMETPSIKGLYYRRVRKVGAL	hKv6.2
1	MPMSSRDRDLHPGHHHFGSCSPLSQLWPGP-EPKSVKGLYYSRARKVGNQ	mKv6.2
51	DASPVDLKKEILINVGGRRYLLPWSTLDRFPLSRLSKLRLCRSYEEIVQL	hKv6.2
51	DASPEANLKEILVNVGGORYLLPWSTLDAFPLSRLSKLRLCRSHEEITQL	mKv6.2
	CDDYDEDSQEFFFDRSPSAFGVIVSFLAAGKLVLLQEMCALSFQEELAYW CDDYDEDSQEFFFDRNPSAFGVIVSFLAAGKLVLLREMCALSFREELSYW	hKv6.2 mKv6.2
151	GIEÐAHLERCCLRKLIRKLEELEELAKUHREDVLRQQRETRRPASHSS	hKv6.2
150	GIEÐTNLERCCLRKLIKKLEÐAAELRREÐAAQRQQQRQACHSEVQAS	mKv6.2
199	RWGLCMNRLREMVENPQSGLPGKVFACLSILFVATTAVSLCVSTMPDLRA	hKv6.2
197	RWARSMNQLREMVEDPQSGLPGKVFACLSVLFVATTAVSLCVSTMPDFRA	mKv6.2
249	EEDQGEGSRKCYYIFIVETICVAWFSLEFCLRFVQAQDKCQFFQGPLNII	hKv6.2
247	EEGKGECTRKCYYIFWVESICVAWFSLEFCLRFVQAPNKCQFFRGPLNVI	mKv6.2
299	DILAISPYYVSLAVSEEPPEDGERPSRSSLYEKVGLVLRVLRALRILYVM	hKv6.2
297	DILAISPYYVSLAVSDESPEAGERPSSSSLYEKVGLVLRVLRALRILYVM	mKv6.2
349	RLARHSLGLQTLGLTVRRCTCEFGLLLLFLAVAITLFSPLVYVAEKESGR	hKv6.2
347	RLARHSLGLQTLGLTVRRCAREFGLLMLFLAVAVTLFSPLVYVAENESGR	mKv6.2
399	VLEFTSIPASYWWAIISMTTVGYGDMVPRSVPGQMVALSSILSGILIMAF	hKv6.2
387	VLEFTSIPASYWWAIISMTTVGYGDMVPRSVPGQMVALSSILSGILIMAF	mKv6.2
449 447	PATSIFHTFSHSYLELKKEQEQLQARLRHLQNTGPASECELLDPHVASEH PATSIFHTFSHSYLELKREQEQVQARLRRLQNTNSASER	hKv6.2 mKv6.2
499	ELMNDVNDLILEGPALPIMHM	hKv6.2
486	ELLSDVDDLVPEGLTSPGRYM	mKv6.2

FIG. 1.

